UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/846,456	05/02/2001	Marie-Francoise Rosier-Montus	ST00015 US NP	1457

5487   7590   07/31/2007
ROSS J. OEHLER
SANOFI-AVENTIS U.S. LLC
1041 ROUTE 202-206
MAIL CODE: D303A
BRIDGEWATER, NJ 08807

EXAMINER
SULLIVAN, DANIEL M

ART UNIT	PAPER NUMBER
1636	

NOTIFICATION DATE	DELIVERY MODE
07/31/2007	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

USPatent.E-Filing@sanofi-aventis.com
andrea.ryan@sanofi-aventis.com

PTOL-90A (Rev. 04/07)

	Application No.	Applicant(s)
Office Action Summary	09/846,456	ROSIER-MONTUS ET AL.
	Examiner	Art Unit	
	Daniel M. Sullivan	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *12 July 2007*.

2a)☐ This action is **FINAL.**   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,3,7-12,33-36 and 57-60* is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3,33-36 and 57-60* is/are rejected.

7)☒ Claim(s) *7-12* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All   b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☒ Notice of References Cited (PTO-892)

2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3)☐ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date _____.

4)☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____ .

5)☐ Notice of Informal Patent Application

6)☒ Other: *See Continuation Sheet*.

Continuation of Attachment(s) 6). Other: SEQUENCE SEARCH RESULTS 09/846,456.

DETAILED ACTION

This Office Action is a reply to the Paper filed 12 July 2007 in response to the Non-Final Office Action mailed 14 February 2007. Claims 1-3, 5-14, 33-38, 57-60 were considered in the 14 February Office Action. Claims 2, 5, 6, 37 and 38 were cancelled in the 12 July Paper. Claims 1, 3, 7-12, 33-36 and 57-60 are pending and under consideration. Finality of the previous Office Action is withdrawn in view of the new grounds for rejection set forth herein below.

Response to Amendment and Arguments

Rejection of claims 2, 5, 6, 37 and 38 is rendered moot by the cancellation thereof.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Rejection of claim 10 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite in reciting, "ranging from nucleotide 1 at position -1" is withdrawn in view of the claim amendment.

New Grounds

Claim Objections

Claim 57 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the

claim(s) in independent form. Claim 57 is directed to the isolated nucleic acid of claim 1,

comprising at least 20 consecutive nucleotides of the sequence SEQ ID NO: 3 or the complement

of SEQ ID NO: 3. Claim 1 is directed to an isolated nucleic acid comprising 500 or more

consecutive nucleotides of SEQ ID NO: 1 or the complement of SEQ ID NO: 1.

As shown in the alignment of SEQ ID NO: 1 and SEQ ID NO: 3 attached hereto (us-09-846-

456a-1.rnpbm, RESULT 7; page 8), SEQ ID NO: 3 comprises all but the final 338 bases of SEQ

ID NO: 1. Therefore, any sequence comprising 500 or more consecutive nucleotides of SEQ ID

NO: 1 must, at a minimum, comprise 162 bases of SEQ ID NO: 3. Therefore, all sequences

within the scope of claim 1 must comprise more than 20 bases of SEQ ID NO: 3 and,

consequently, claim 57 fails to further limit the subject matter of claim 1.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the

basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claims 1, 3, 33-36 and 57-60 are rejected under 35 U.S.C. 102(a) as being anticipated by

NCBI Entrez Nucleotide Database entry AC012230.2 (19 November 1999),

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=6454033, downloaded 25 July 2007 as

evidenced by Osoegawa et al. (2001) *Genome Res.* 11:483-496.

Claim 1 is directed to an isolated nucleic acid comprising a polynucleotide having 500 or

more consecutive nucleotides of the nucleotide sequence SEQ ID NO: 1 and claim 3 is directed

to an isolated nucleic acid comprising a polynucleotide having at least 200 consecutive

nucleotides of the sequence SEQ ID NO: 3. Claim 57 is directed to the nucleic acid of claim 1,

wherein the nucleic acid comprises at least 20 consecutive nucleotides of SEQ ID NO: 3.

The AC012230 entry teaches a nucleic acid comprising a 540 base sequence that is

identical to nucleotides 2130-2670 of SEQ ID NO: 1 and 3. (See the alignment of SEQ ID NO: 3

with the AC012230 entry on the attached sequence search results (us-09-846-456a-3.oli.rge,

RESULT 11). Note that the sequence at nucleotides 2130-2670 of SEQ ID NO: 1 is identical to

the sequence of SEQ ID NO: 3 (see us-09-846-456a-1.rnpbm, RESULT 7; page 8 of the attached

sequence search). Also note that the alignment on the sequence search is numbered according to

version 3 of the AC012230 entry while the cited art is version 2 (i.e., AC012230.2). The

corresponding sequence is begins at 2703 and continues through 3243 of the AC012230.2

sequence.

The AC012230 entry anticipates the limitations of the instant claims 1, 3 and 57. In

addition, the AC012230 nucleic acid further comprises additional sequence which is "of interest"

according to the limitations of claim 33 and would additionally comprise sequence that is in the

sense and antisense orientation with respect to the promoter comprised by the nucleic acid, as

well as sense and antisense sequences of interest comprised by the BAC vector itself, according

to the limitations of claim 34. Claim 58 recites that the isolated nucleic acid further comprises 35

or more consecutive nucleotides of SEQ ID NO: 5 or the complement of SEQ ID NO: 5. This

limitation is met by, for example, the sequence from 147555-147614 of the AC012230.2

sequence, which is 100% complementary to the sequence from nucleotide 100 to nucleotide 159

of SEQ ID NO: 5.

Finally, the AC012230 entry teaches that the sequence is comprised in an RP11 clone

(a.k.a., RPC-11; see under "DEFINITION"). Osoegawa et al. teaches that RPCI-11 is a BAC

library. (See especially page 492, second sentence of the "DISCUSSION".) In view of the fact

that nucleic acids in BAC libraries are comprised within vectors and propagated in bacteria, the

cloning vector of claims 35 and 36 and isolated host cell of claims 59 and 60 are inherent to the

teaching of the nucleic acid comprised in an RP11 clone as disclosed in the AC012230.

Database entry AC012230, as evidenced by Osoegawa et al., teaches all of the limitations

of the instant claims. Therefore, the claims are anticipated by the prior art.

Allowable Subject Matter

Claims 7-12 are objected to as being dependent upon a rejected base claim, but would be

allowable if rewritten in independent form including all of the limitations of the base claim and

any intervening claims.

Conclusion

Any inquiry concerning this communication or earlier communications from the
examiner should be directed to Daniel M. Sullivan whose telephone number is 571-272-0779.
The examiner can normally be reached on Monday through Friday 6:30-3:00.
If attempts to reach the examiner by telephone are unsuccessful, the examiner's
supervisor, Joseph Woitach, Ph.D. can be reached on 571-272-0739. The fax phone number for
the organization where this application or proceeding is assigned is 571-273-8300.
Information regarding the status of an application may be obtained from the Patent
Application Information Retrieval (PAIR) system. Status information for published applications
may be obtained from either Private PAIR or Public PAIR. Status information for unpublished
applications is available through Private PAIR only. For more information about the PAIR
system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR
system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).
Patent applicants with problems or questions regarding electronic images that can be
viewed in the Patent Application Information Retrieval system (PAIR) (http://pair-

direct.uspto.gov) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Daniel M. Sullivan, Ph.D.
Primary Examiner
Art Unit 1636

SEQUENCE SEARCH RESULTS 09/846,456

us-09-846-456a-3..oli.rge

RESULT 11
AC012230

```
LOCUS       AC012230              175064 bp    DNA      linear   HTG 22-APR-2000
DEFINITION  Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
            pieces.
ACCESSION   AC012230.
VERSION     AC012230.3  GI:7637254
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175064)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-1M10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 175064)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Apr 22, 2000 this sequence version replaced gi:6454033.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L2510
                Center clone name: 1_M_10
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 117571 bases at least Q40
                Consensus quality: 145749 bases at least Q30
                Consensus quality: 160940 bases at least Q20
                Insert size: 185000; agarose-fp
                Insert size: 171264; sum-of-contigs
                Quality coverage: 2.9 in Q20 bases; agarose-fp
                Quality coverage: 3.2 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 39 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *         1     1003: contig of 1003 bp in length
```

1

```
*     1004     1103: gap of 100 bp
*     1104     2634: contig of 1531 bp in length
*     2635     2734: gap of 100 bp
*     2735     4415: contig of 1681 bp in length
*     4416     4515: gap of 100 bp
*     4516     5785: contig of 1270 bp in length
*     5786     5885: gap of 100 bp
*     5886     7879: contig of 1994 bp in length
*     7880     7979: gap of 100 bp
*     7980     9686: contig of 1707 bp in length
*     9687     9786: gap of 100 bp
*     9787    12253: contig of 2467 bp in length
*    12254    12353: gap of 100 bp
*    12354    15228: contig of 2875 bp in length
*    15229    15328: gap of 100 bp
*    15329    17200: contig of 1872 bp in length
*    17201    17300: gap of 100 bp
*    17301    20131: contig of 2831 bp in length
*    20132    20231: gap of 100 bp
*    20232    22587: contig of 2356 bp in length
*    22588    22687: gap of 100 bp
*    22688    25707: contig of 3020 bp in length
*    25708    25807: gap of 100 bp
*    25808    28184: contig of 2377 bp in length
*    28185    28284: gap of 100 bp
*    28285    31338: contig of 3054 bp in length
*    31339    31438: gap of 100 bp
*    31439    34299: contig of 2861 bp in length
*    34300    34399: gap of 100 bp
*    34400    38318: contig of 3919 bp in length
*    38319    38418: gap of 100 bp
*    38419    42835: contig of 4417 bp in length
*    42836    42935: gap of 100 bp
*    42936    45448: contig of 2513 bp in length
*    45449    45548: gap of 100 bp
*    45549    48116: contig of 2568 bp in length
*    48117    48216: gap of 100 bp
*    48217    52618: contig of 4402 bp in length
*    52619    52718: gap of 100 bp
*    52719    56592: contig of 3874 bp in length
*    56593    56692: gap of 100 bp
*    56693    59635: contig of 2943 bp in length
*    59636    59735: gap of 100 bp
*    59736    63661: contig of 3926 bp in length
*    63662    63761: gap of 100 bp
*    63762    68437: contig of 4676 bp in length
*    68438    68537: gap of 100 bp
*    68538    71458: contig of 2921 bp in length
*    71459    71558: gap of 100 bp
*    71559    76888: contig of 5330 bp in length
*    76889    76988: gap of 100 bp
*    76989    82113: contig of 5125 bp in length
*    82114    82213: gap of 100 bp
*    82214    88220: contig of 6007 bp in length
*    88221    88320: gap of 100 bp
*    88321    93499: contig of 5179 bp in length
*    93500    93599: gap of 100 bp
*    93600    97901: contig of 4302 bp in length
*    97902    98001: gap of 100 bp
*    98002   103016: contig of 5015 bp in length
*   103017   103116: gap of 100 bp
*   103117   109178: contig of 6062 bp in length
*   109179   109278: gap of 100 bp
*   109279   117307: contig of 8029 bp in length
*   117308   117407: gap of 100 bp
*   117408   124079: contig of 6672 bp in length
*   124080   124179: gap of 100 bp
*   124180   131281: contig of 7102 bp in length
*   131282   131381: gap of 100 bp
*   131382   138059: contig of 6678 bp in length
*   138060   138159: gap of 100 bp
```

2

```
              *     138160    145491: contig of 7332 bp in length
              *     145492    145591: gap of 100 bp
              *     145592    157391: contig of 11800 bp in length
              *     157392    157491: gap of 100 bp
              *     157492    175064: contig of 17573 bp in length.
FEATURES                 Location/Qualifiers
     source              1. .175064
                         /organism="Homo sapiens"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:9606"
                         /clone="RP11-1M10"
                         /clone_lib="RPCI-11 Human Male BAC"
     misc_feature        1. .1003
                         /note="assembly_fragment"
     misc_feature        1104. .2634
                         /note="assembly_fragment"
     misc_feature        2735. .4415
                         /note="assembly_fragment"
     misc_feature        4516. .5785
                         /note="assembly_fragment"
     misc_feature        5886. .7879
                         /note="assembly_fragment"
     misc_feature        7980. .9686
                         /note="assembly_fragment"
     misc_feature        9787. .12253
                         /note="assembly_fragment"
     misc_feature        12354. .15228
                         /note="assembly_fragment"
     misc_feature        15329. .17200
                         /note="assembly_fragment"
     misc_feature        17301. .20131
                         /note="assembly_fragment"
     misc_feature        20232. .22587
                         /note="assembly_fragment"
     misc_feature        22688. .25707
                         /note="assembly_fragment"
     misc_feature        25808. .28184
                         /note="assembly_fragment"
     misc_feature        28285. .31338
                         /note="assembly_fragment"
     misc_feature        31439. .34299
                         /note="assembly_fragment"
     misc_feature        34400. .38318
                         /note="assembly_fragment"
     misc_feature        38419. .42835
                         /note="assembly_fragment"
     misc_feature        42936. .45448
                         /note="assembly_fragment"
     misc_feature        45549. .48116
                         /note="assembly_fragment"
     misc_feature        48217. .52618
                         /note="assembly_fragment"
     misc_feature        52719. .56592
                         /note="assembly_fragment"
     misc_feature        56693. .59635
                         /note="assembly_fragment"
     misc_feature        59736. .63661
                         /note="assembly_fragment"
     misc_feature        63762. .68437
                         /note="assembly_fragment"
     misc_feature        68538. .71458
                         /note="assembly_fragment
                         clone_end:SP6
                         vector_side:left"


  Query Match          18.7%;   Score 541;   DB 2;   Length 175064;
  Best Local Similarity   100.0%;   Pred. No. 2.4e-294;
  Matches  541;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     2130 TTTGTTTGTTTCTTTTTTTGTTTTTGTGGCCTCCTTCCTCTCAATTTATGAAGAGAAGCA 2189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

3

```
Db      2903 TTTGTTTGTTTCTTTTTTTGTTTTTGTGGCCTCCTTCCTCTCAATTTATGAAGAGAAGCA 2962

Qy      2190 GTAAGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAA 2249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2963 GTAAGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAA 3022

Qy      2250 GGCAGTAGGTCGCCTATCAAAAATCAAAGTCCAGGTTTGTGGGGGGAAAACAAAAGCAGC 2309
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3023 GGCAGTAGGTCGCCTATCAAAAATCAAAGTCCAGGTTTGTGGGGGGAAAACAAAAGCAGC 3082

Qy      2310 CCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAAC 2369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3083 CCATTACCCAGAGGACTGTCCGCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAAC 3142

Qy      2370 AAAAGACAAGACAAAATGATTGGCGTCCTGAGGGAGATTCAGCCTAGAGCTCTCTCTCCC 2429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3143 AAAAGACAAGACAAAATGATTGGCGTCCTGAGGGAGATTCAGCCTAGAGCTCTCTCTCCC 3202

Qy      2430 CCAATCCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAAAATTGCGGAAAGCAGGA 2489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3203 CCAATCCCTCCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAAAATTGCGGAAAGCAGGA 3262

Qy      2490 TTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCT 2549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3263 TTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCT 3322

Qy      2550 GCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGCGGGCCCGGGCGGGG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3323 GCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCGTCTTAGGCCGGCGGGCCCGGGCGGGG 3382

Qy      2610 GAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCCACC 2669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3383 GAAGGGGACGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCCACCCCACC 3442

Qy      2670 C 2670
             |
Db      3443 C 3443
```

vg-009-846-A56a/v. PPPPT

```
RESULT 12
AC012230/c
LOCUS           AC012230                175064 bp    DNA     linear   HTG 22-APR-2000
DEFINITION      Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
                pieces.
ACCESSION       AC012230
VERSION         AC012230.3  GI:7637254
KEYWORDS        HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 175064)
  AUTHORS       Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE         Homo sapiens, clone RP11-1M10
  JOURNAL       Unpublished
REFERENCE       2  (bases 1 to 175064)
  AUTHORS       Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
                Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
                Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
                Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
                Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
                Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
                Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
                McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
                Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
                Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
```

4

```
              Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
              Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
              Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE       Direct Submission
  JOURNAL     Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
              Research, 320 Charles Street, Cambridge, MA 02141, USA
  COMMENT     On Apr 22, 2000 this sequence version replaced gi:6454033.
              All repeats were identified using RepeatMasker:
              Smit, A.F.A. & Green, P. (1996-1997)
              http://ftp.genome.washington.edu/RM/RepeatMasker.html
              -------------- Genome Center
                  Center: Whitehead Institute/ MIT Center for Genome Research
                  Center code: WIBR
                  Web site: http://www-seq.wi.mit.edu
                  Contact: sequence_submissions@genome.wi.mit.edu
              -------------- Project Information
                  Center project name: L2510
                  Center clone name: 1_M_10
              -------------- Summary Statistics
                  Sequencing vector: M13; M77815; 100% of reads
                  Chemistry: Dye-terminator Big Dye; 100% of reads
                  Assembly program: Phrap; version 0.960731
                  Consensus quality: 117571 bases at least Q40
                  Consensus quality: 145749 bases at least Q30
                  Consensus quality: 160940 bases at least Q20
                  Insert size: 185000; agarose-fp
                  Insert size: 171264; sum-of-contigs
                  Quality coverage: 2.9 in Q20 bases; agarose-fp
                  Quality coverage: 3.2 in Q20 bases; sum-of-contigs
              --------------.
              * NOTE: This is a 'working draft' sequence. It currently
              * consists of 39 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *         1     1003: contig of 1003 bp in length
              *      1004     1103: gap of 100 bp
              *      1104     2634: contig of 1531 bp in length
              *      2635     2734: gap of 100 bp
              *      2735     4415: contig of 1681 bp in length
              *      4416     4515: gap of 100 bp
              *      4516     5785: contig of 1270 bp in length
              *      5786     5885: gap of 100 bp
              *      5886     7879: contig of 1994 bp in length
              *      7880     7979: gap of 100 bp
              *      7980     9686: contig of 1707 bp in length
              *      9687     9786: gap of 100 bp
              *      9787    12253: contig of 2467 bp in length
              *     12254    12353: gap of 100 bp
              *     12354    15228: contig of 2875 bp in length
              *     15229    15328: gap of 100 bp
              *     15329    17200: contig of 1872 bp in length
              *     17201    17300: gap of 100 bp
              *     17301    20131: contig of 2831 bp in length
              *     20132    20231: gap of 100 bp
              *     20232    22587: contig of 2356 bp in length
              *     22588    22687: gap of 100 bp
              *     22688    25707: contig of 3020 bp in length
              *     25708    25807: gap of 100 bp
              *     25808    28184: contig of 2377 bp in length
              *     28185    28284: gap of 100 bp
              *     28285    31338: contig of 3054 bp in length
              *     31339    31438: gap of 100 bp
              *     31439    34299: contig of 2861 bp in length
              *     34300    34399: gap of 100 bp
              *     34400    38318: contig of 3919 bp in length
              *     38319    38418: gap of 100 bp
              *     38419    42835: contig of 4417 bp in length
```

```
*        42836      42935: gap of 100 bp
*        42936      45448: contig of 2513 bp in length
*        45449      45548: gap of 100 bp
*        45549      48116: contig of 2568 bp in length
*        48117      48216: gap of 100 bp
*        48217      52618: contig of 4402 bp in length
*        52619      52718: gap of 100 bp
*        52719      56592: contig of 3874 bp in length
*        56593      56692: gap of 100 bp
*        56693      59635: contig of 2943 bp in length
*        59636      59735: gap of 100 bp
*        59736      63661: contig of 3926 bp in length
*        63662      63761: gap of 100 bp
.*       63762      68437: contig of 4676 bp in length
*        68438      68537: gap of 100 bp
*        68538      71458: contig of 2921 bp in length
*        71459      71558: gap of 100 bp
*        71559      76888: contig of 5330 bp in length
*        76889      76988: gap of 100 bp
*        76989      82113: contig of 5125 bp in length
*        82114      82213: gap of 100 bp
*       ·82214      88220: contig of 6007 bp in length
*        88221      88320: gap of 100 bp
*        88321      93499: contig of 5179 bp in length
.*       93500      93599: gap of 100 bp
*        93600      97901: contig of 4302 bp in length
*        97902      98001: gap of 100 bp
*        98002     103016: contig of 5015 bp in length
*       103017     103116: gap of 100 bp
*       103117     109178: contig of 6062 bp in length
*       109179     109278: gap of 100 bp
*       109279     117307: contig of 8029 bp in length
*       117308     117407: gap of 100 bp
*       117408     124079: contig of 6672 bp in length
*       124080     124179: gap of 100 bp
*       124180     131281: contig of 7102 bp in length
*       131282     131381: gap of 100 bp
*       131382     138059: contig of 6678 bp in length·
*       138060     138159: gap of 100 bp
*       138160     145491: contig of 7332 bp in length
*       145492     145591: gap of 100 bp
*  ·    145592     157391: contig of 11800 bp in length
*       157392     157491: gap of 100 bp
*       157492     175064: contig of 17573 bp in length.
FEATURES             Location/Qualifiers
    source           1. .175064
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="RP11-1M10"
                     /clone_lib="RPCI-11 Human Male BAC"
    misc_feature     1. .1003
                     /note="assembly_fragment"
    misc_feature     1104. .2634
                     /note="assembly_fragment"
    misc_feature     2735. .4415
                     /note="assembly_fragment"
    misc_feature     4516. .5785
                     /note="assembly_fragment"
    misc_feature     5886. .7879
                     /note="assembly_fragment"
    misc_feature     7980. .9686
                     /note="assembly_fragment"
    misc_feature     9787. .12253
                     /note="assembly_fragment"
    misc_feature     12354. .15228
                     /note="assembly_fragment"
    misc_feature     15329. .17200
                     /note="assembly_fragment"
    misc_feature     17301. .20131
                     /note="assembly_fragment"
```

6

```
        misc_feature      20232. .22587
                          /note="assembly_fragment"
        misc_feature      22688. .25707
                          /note="assembly_fragment"
        misc_feature      25808. .28184
                          /note="assembly_fragment"
        misc_feature      28285. .31338
                          /note="assembly_fragment"
        misc_feature      31439. .34299
                          /note="assembly_fragment"
        misc_feature      34400. .38318
                          /note="assembly_fragment"
        misc_feature      38419. .42835
                          /note="assembly_fragment"
        misc_feature      42936. .45448
                          /note="assembly_fragment"
        misc_feature      45549. .48116
                          /note="assembly_fragment"
        misc_feature      48217. .52618
                          /note="assembly_fragment"
        misc_feature      52719. .56592
                          /note="assembly_fragment"
        misc_feature      56693. .59635
                          /note="assembly_fragment"
        misc_feature      59736. .63661
                          /note="assembly_fragment"
        misc_feature      63762. .68437
                          /note="assembly_fragment"
        misc_feature      68538. .71458
                          /note="assembly_fragment
                          clone_end:SP6
                          vector_side:left"

   Query Match              11.9%;  Score 344;  DB 2;  Length 175064;
   Best Local Similarity    99.7%;  Pred. No. 1.3e-182;
   Matches  394;  Conservative   0;  Mismatches    1;  Indels   0;  Gaps   0;

Qy      35 TACTCGGGAGGTGGAGGTTGCAATGAGCCCAGATCGCACCATTGCACTCCAGCCTGGGCA 94
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1645 TACTCGGGAGGTGGAGGTTGCAATGAGCCCAGATCGCACCATTGCACTCCAGCCTGGGCA 1586

Qy      95 ACAAAAGGTGAAACTCCATCTCAATTAAAAAAAAAAAGAATGATTTTGGTGGTCGACTTCA 154
           ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    1585 ACAAAAGGTGAAACTCCATCTCAATTAAAAAAAAAAATAATGATTTTGGTGGTCGACTTCA 1526

Qy     155 AATAGGTAGGAGAAGAAGGAGAGAGGAGATGGAGGGTCAGGGAGATCTAATTACTCTCTA 214
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1525 AATAGGTAGGAGAAGAAGGAGAGAGGAGATGGAGGGTCAGGGAGATCTAATTACTCTCTA 1466

Qy     215 AAATCATGCTAGGAAAGATAACACCTTTTAATAACACTCTCTGCTTTTATAACATCATTC 274
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1465 AAATCATGCTAGGAAAGATAACACCTTTTAATAACACTCTCTGCTTTTATAACATCATTC 1406

Qy     275 TGCCAAGGAGCTCAAAGGTTTCAACAAAGTTCACTTTCAGAAAACCCCTTTGAGGAAGAC 334
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1405 TGCCAAGGAGCTCAAAGGTTTCAACAAAGTTCACTTTCAGAAAACCCCTTTGAGGAAGAC 1346

Qy     335 AGAATATACATCTTCTCTCCATTTTAAAGATGAAGAAACAGGCCGGGCACAATGGCTAAT 394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1345 AGAATATACATCTTCTCTCCATTTTAAAGATGAAGAAACAGGCCGGGCACAATGGCTAAT 1286

Qy     395 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCA 429
           |||||||||||||||||||||||||||||||||||
Db    1285 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCA 1251
```

7

us-09-846-456a-1.rnpbm

RESULT 7
US-09-846-456-3
; Sequence 3, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denefle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: Fojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying Its
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 2893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-846-456-3

  Query Match   89.5%; Score 2893; DB 3; Length 2893;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 2893; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ACAGGGCATGGTGGCAGGTGCCTGTAATCTCAGTTACTCGGGAGGTGGAGGTTGCAATGA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACAGGGCATGGTGGCAGGTGCCTGTAATCTCAGTTACTCGGGAGGTGGAGGTTGCAATGA 60

Qy   61 GCCCAGATCGCACCATTGCACTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCCCAGATCGCACCATTGCACTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATT 120

Qy   121 AAAAAAAAAAGAATGATTTTGGTGGTCGACTTCAAATAGGTAGGAGAAGAAGGAGAGAGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAAAAAAAAGAATGATTTTGGTGGTCGACTTCAAATAGGTAGGAGAAGAAGGAGAGAGG 180

Qy   181 AGATGGAGGGTCAGGGAGATCTAATTACTCTCTAAAATCATGCTAGGAAAGATAACACCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGATGGAGGGTCAGGGAGATCTAATTACTCTCTAAAATCATGCTAGGAAAGATAACACCT 240

Qy   241 TTTAATAACACTCTCTGCTTTTATAACATCATTCTGCCAAGGAGCTCAAAGGTTTCAACA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTAATAACACTCTCTGCTTTTATAACATCATTCTGCCAAGGAGCTCAAAGGTTTCAACA 300

Qy   301 AAGTTCACTTTCAGAAAACCCCTTTGAGGAAGACAGAATATACATCTTCTCTCCATTTTA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAGTTCACTTTCAGAAAACCCCTTTGAGGAAGACAGAATATACATCTTCTCTCCATTTTA 360

Qy   361 AAGATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AAGATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGG 420

Qy   421 CTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAA 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAA 480

Qy   481 ACCCTGTCTCTACAAAAAAAATACAAAAATTAGATGGGTGTGGTGGCATGCACCTGTGGT 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACCCTGTCTCTACAAAAAAAATACAAAAATTAGATGGGTGTGGTGGCATGCACCTGTGGT 540

8

```
Qy    541 CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCTACA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCTACA 600

Qy    601 CTGAGCCATGATTGGATCACTGCACTCCAGCCTGGGTAGACAGAGCAAGACCCTGTCTCA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGAGCCATGATTGGATCACTGCACTCCAGCCTGGGTAGACAGAGCAAGACCCTGTCTCA 660

Qy    661 AAAAAAAGAAATGAAAGAGAAAGAAAGAAAGAGGAGAGGAGAGGAGATGAGGGGAGGAGG 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAAAAAGAAATGAAAGAGAAAGAAAGAAAGAGGAGAGGAGAGGAGATGAGGGGAGGAGG 720

Qy    721 GAGGGGGGGAGGAAGGAAGGAAGGAAGGAAGGAAAAAAAGATGAAAAAAGAAAAAAACAA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAGGGGGGGAGGAAGGAAGGAAGGAAGGAAGGAAAAAAAGATGAAAAAAGAAAAAAACAA 780

Qy    781 GATGAAACAGAGGCAGAAAGACTTTACGTAAATTGCTCATCATGTGGTTGTCAAGTTTGA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GATGAAACAGAGGCAGAAAGACTTTACGTAAATTGCTCATCATGTGGTTGTCAAGTTTGA 840

Qy    841 CCCCAAAACCCAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGGTCCGCTCT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCCCAAAACCCAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAGGGGGTCCGCTCT 900

Qy    901 CCTGGGCCTTGGGCTTTAGAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCTTT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCTGGGCCTTGGGCTTTAGAAAGCTCATCTCTGGCCTTTCTGAGATCCATCCCTTTCTTT 960

Qy    961 TTATTTTTCTTGACACGGAGTCTTGCTCTGTCACTCAGGCTGGAGTGCAGTGGCATGATC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTATTTTTCTTGACACGGAGTCTTGCTCTGTCACTCAGGCTGGAGTGCAGTGGCATGATC 1020

Qy   1021 TCGACTCACTGTAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TCGACTCACTGTAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGA 1080

Qy   1081 GATAACAGGCGCCCGCCACCACATCTGGCTAATTTTTGTATTTTTAGTAAAGACTGGGTT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GATAACAGGCGCCCGCCACCACATCTGGCTAATTTTTGTATTTTTAGTAAAGACTGGGTT 1140

Qy   1141 TCATCATGTTGGCCAGGTTGGTTTCGAACTCCTGACCTGAGGTGAGCTGCCCACCTTGGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCATCATGTTGGCCAGGTTGGTTTCGAACTCCTGACCTGAGGTGAGCTGCCCACCTTGGC 1200

Qy   1201 CTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGCTCAGATCCATCCCTTT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGCTCAGATCCATCCCTTT 1260

Qy   1261 CTAAGGGCAAACAGTCCATGGTGCAAAGGGGCCATGCCACCCAGAGTTATGAGTACCTGG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CTAAGGGCAAACAGTCCATGGTGCAAAGGGGCCATGCCACCCAGAGTTATGAGTACCTGG 1320

Qy   1321 GACTCCAGAATTCCTTGCCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGGCCTC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GACTCCAGAATTCCTTGCCTGGTGGCCTCCACATGCACTTCCAGGGCCTGCTTGGGCCTC 1380

Qy   1381 TTCTATGCGTCTGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCC 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTCTATGCGTCTGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCC 1440

Qy   1441 GTGGCCTGGAGATCCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGCTGAATGTCTGCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTGGCCTGGAGATCCTGTTGACTGTAGCATGGAGGGGGCTTGTGCAGCTGAATGTCTGCA 1500

Qy   1501 TGCAGGTGGTGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAGAGAAGTAGGCTTG 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGCAGGTGGTGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAGAGAAGTAGGCTTG 1560

Qy   1561 GGGCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

9

```
Db     1561 GGGCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCT 1620

Qy     1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGACCTT 1680

Qy     1681 GTGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GTGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 1740

Qy     1741 CTTCTATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTT 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CTTCTATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTT 1800

Qy     1801 TGGCCAGAATAAGGTGACATTTAGTTTGTTGGCTTGATGGATGACTTAAATATTTAGACA 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 TGGCCAGAATAAGGTGACATTTAGTTTGTTGGCTTGATGGATGACTTAAATATTTAGACA 1860

Qy     1861 TGGTGTGTAGGCCTGCATTCCTACTCTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGT 1920
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 TGGTGTGTAGGCCTGCATTCCTACTCTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGT 1920

Qy     1921 AGTTTTGCTCCCCTACAGCCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACAT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 AGTTTTGCTCCCCTACAGCCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACAT 1980

Qy     1981 AATTTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 AATTTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA 2040

Qy     2041 GTCCTGTGTTTTTATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTC 2100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 GTCCTGTGTTTTTATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTC 2100

Qy     2101 CATATTGTTCTGTGTTTTTGTTTGTTTGTTTGTTTGTTTCTTTTTTTGTTTTTGTGGCC 2160
            |||||||||||||||||||||||||.||||||||||||||||||||||||||||||||||
Db     2101 CATATTGTTCTGTGTTTTTGTTTGTTTGTTTGTTTGTTTCTTTTTTTGTTTTTGTGGCC 2160

Qy     2161 TCCTTCCTCTCAATTTATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGA 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 TCCTTCCTCTCAATTTATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGA 2220

Qy     2221 CCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAAATCAAAGTC 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 CCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAAATCAAAGTC 2280

Qy     2281 CAGGTTTGTGGGGGGAAAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCT 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 CAGGTTTGTGGGGGGAAAACAAAAGCAGCCCATTACCCAGAGGACTGTCCGCCTTCCCCT 2340

Qy     2341 CACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGCGTCCTGA 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 CACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGCGTCCTGA 2400

Qy     2401 GGGAGATTCAGCCTAGAGCTCTCTCTCCCCCAATCCCTCCCTCCGGCTGAGGAAACTAAC 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 GGGAGATTCAGCCTAGAGCTCTCTCTCCCCCAATCCCTCCCTCCGGCTGAGGAAACTAAC 2460

Qy     2461 AAAGGAAAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTT 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 AAAGGAAAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTT 2520

Qy     2521 GGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGC 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 GGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGC 2580

Qy     2581 GCGTCTTAGGCCGGCGGGCCCGGGCGGGGGAAGGGGACGCAGACCGCGGACCCTAAGACA 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 GCGTCTTAGGCCGGCGGGCCCGGGCGGGGGAAGGGGACGCAGACCGCGGACCCTAAGACA 2640

Qy     2641 CCTGCTGTACCCTCCACCCCCACCCCACCCCACCCACCTCCCCCCAACTCCCTAGATGTG 2700
```

10

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641  CCTGCTGTACCCTCCACCCCCACCCCACCCCACCCACCTCCCCCCAACTCCCTAGATGTG  2700

Qy      2701  TCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGC  2760
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701  TCGTGGGCGGCTGAACGTCGCCCGTTTAAGGGGCGGGCCCCGGCTCCACGTGCTTTCTGC  2760

Qy      2761  TGAGTGACTGAACTACATAAACAGAGGCCGGGAAGGGGGCGGGGAGGAGGGAGAGCACAG  2820
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761  TGAGTGACTGAACTACATAAACAGAGGCCGGGAAGGGGGCGGGGAGGAGGGAGAGCACAG  2820

Qy      2821  GCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCC  2880
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821  GCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCC  2880

Qy      2881  CGGCAAAAACCCC  2893
                 |||||||||||||
Db      2881  CGGCAAAAACCCC  2893
```

11